

SEQUENCE LISTING

<110> Hodge, Martin R.

<120> Novel IL-9/IL-2 Receptor-Like Molecules
and Uses Thereof

<130> 5800-17A

<150> US 09/313,913
<151> 1999-05-18

<160> 8

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2343

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (349)...(1962)

<400> 1

gtggctgaca	gccacgcagc	tgtgtctgtc	tgtctgcggc	ccgtgcattcc	ctgctgcggc	60
cgcctggta	c	tttccttgc	gtctcttcc	tctgtctgt	gctctgtgg	120
ggaggcccag	ctggccgtca	tcaagatgtac	aggcttatg	acagcctgtat	tggactcg	180
ggctgggtgt	ggattctcac	cccaggcctc	tgccgtctt	ctcagaccct	catctgtcac	240
ccccacgctg	aaccagctg	ccacccca	aagccatca	gactgcccc	agcacacgga	300
atggatttct	gagaagaag	ccgaaacaga	aggccgtgg	gagtca	atg ccg cgt	357
					Met Pro Arg	
				1		

ggc tgg gcc	ccc ctg	ctc ctg	ctg ctc	cag gga	ggc tgg ggc	405
Gly Trp Ala	Ala Pro	Leu Leu	Leu Leu	Leu Leu	Gln Gly Gly Trp Gly	
5	10			15		

tgc ccc gac	ctc gtc	tgc tac	acc gat	tac ctc	cag acg	gtc atc tgc	453
Cys Pro Asp	Leu Val	Cys Tyr	Thr Asp	Tyr Leu	Gln Thr Val	Ile Cys	
20	25			30		35	

atc ctg gaa atg	tgg aac	ctc cac	ccc agc	acg ctc	acc ctt	acc tgg	501
Ile Leu Glu	Met Trp	Asn Leu	His Pro	Ser Thr	Leu Thr	Leu Thr Trp	
40			45		50		

caa gac cag tat	gaa gag	ctg aag	gac gag	gcc acc	tcc tgc	agc ctc	549
Gln Asp Gln	Tyr Glu	Glu Leu	Lys Asp	Glu Ala	Thr Ser	Cys Ser Leu	
55			60		65		

cac agg tcg	gcc cac	aat gcc	acg cat	gcc acc	acc tac	acc tgc	cac atg	597
His Arg Ser	Ala His	Asn Ala	Thr His	Ala Thr	Tyr Thr	Cys His	Met	
70			75		80			

gat gta ttc	cac ttc	atg gcc	gac gac	att ttc	agt gtc	aac atc aca	645
-------------	---------	---------	---------	---------	---------	-------------	-----

	Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr				
	85	90	95		
	gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt ctc ctg gct			693	
	Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala				
	100	105	110	115	
	gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg acc ttc tca			741	
	Glu Ser Ile Lys Pro Ala Pro Phe Asn Val Thr Val Thr Phe Ser				
	120	125	130		
	gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac cct gcc ttc			789	
	Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe				
	135	140	145		
	tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac ccg			837	
	Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg				
	150	155	160		
	gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc tca gtg gac			885	
	Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp				
	165	170	175		
	tca aga agt gtc tcc ctc ccc ctg gag ttc cgc aaa gac tcg agc			933	
	Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser				
	180	185	190	195	
	tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc tcc tac cag			981	
	Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln				
	200	205	210		
	ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag acc cag tca			1029	
	Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser				
	215	220	225		
	gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt ctc ctc ctg			1077	
	Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu Leu Leu				
	230	235	240		
	ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag acc cat cca			1125	
	Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys Thr His Pro				
	245	250	255		
	ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc cct gag cgg			1173	
	Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser Pro Glu Arg				
	260	265	270	275	
	tcc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc aag aaa tgg			1221	
	Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe Lys Lys Trp				
	280	285	290		
	gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga ccc tgg agc			1269	
	Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly Pro Trp Ser				
	295	300	305		
	cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac cca cca ccg			1317	
	Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His Pro Pro Arg				

DNA sequence

	310	315	320	
agc ccg gcc aag agg ctg cag ctc acg gag cta caa gaa cca gca gag Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu Pro Ala Glu	325	330	335	1365
ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg ccg aca gcc Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp Pro Thr Ala	340	345	350	1413
cag aac tcg ggg ggc tca gct tac agt gag gag agg gat ccg cca tac Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro Tyr	360	365	370	1461
ggc ctg gtg tcc att gac aca gtg act gtg cta gat gca gag ggg cca Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala Glu Gly Pro	375	380	385	1509
tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca gcc ctg gac Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Leu Asp	390	395	400	1557
ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac cca ctc ttg Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp Pro Leu Leu	405	410	415	1605
gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca gct ggc agc Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser Ala Gly Ser	420	425	430	1653
cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga cta aag cca Pro Gly Leu Gly Pro Leu Gly Ser Leu Leu Asp Arg Leu Lys Pro	440	445	450	1701
ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc tgg ggt ggc Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro Trp Gly Gly	455	460	465	1749
cggtca cct gga ggg gtc tca gag agt gag gcg ggc tca ccc ctg gcc Arg Ser Pro Gly Gly Val Ser Glu Ser Ala Gly Ser Pro Leu Ala	470	475	480	1797
ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc tct gac tgc Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly Ser Asp Cys	485	490	495	1845
agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac gaa gga ccc Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp Glu Gly Pro	500	505	510	1893
ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg cca ctt tcg Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro Pro Leu Ser	520	525	530	1941
agc cct gga ccc cag gcc agc taatgaggct gactggatgt ccagagctgg Ser Pro Gly Pro Gln Ala Ser	535			1992

ccaggccact	ggccctgag	ccagagacaa	ggcacctgg	gctgtatgt	gaagacacct	2052
gcagccttg	gtccctgga	tggccttg	agcctatgt	ttacagtgtc	tgtgtgtgt	2112
tgtcatatg	tgtgtgtgt	cataatgtat	tgtgtgtgt	tgtgtgtt	aggcgca	2172
tggcatgtcc	acgtgtgtgt	gtgattgcac	gtgcctgtgg	gcctggata	atgcccattgg	2232
tactccatgc	attcacctgc	cctgtcatgt	tctggactca	cggagctcac	ccatgtgcac	2292
aagtgtgcac	agtaaacgtg	tttgtggta	aaaaaaaaaa	aaaaaaaaaa	a	2343

<210> 2
 <211> 538
 <212> PRT
 <213> Homo sapiens IL-2/IL-9 Receptor Like

<400> 2															
Met	Pro	Arg	Gly	Trp	Ala	Ala	Pro	Leu	Leu	Leu	Leu	Leu	Gln	Gly	
1					5			10					15		
Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	Thr
						20		25					30		
Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr
						35		40				45			
Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser
						50		55			60				
Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr
						65		70			75			80	
Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val
						85			90			95			
Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe
						100		105			110				
Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	Val
						115		120			125				
Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Tyr	Glu	Asp	
						130		135			140				
Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr
						145		150			155			160	
Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile
						165			170			175			
Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Glu	Phe	Arg	Lys	
						180		185			190				
Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser
						195			200			205			
Ser	Tyr	Gln	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln
						210		215			220				
Thr	Gln	Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	Pro	His	Leu	Leu	
						225		230			235			240	
Leu	Leu	Leu	Leu	Val	Ile	Val	Phe	Ile	Pro	Ala	Phe	Trp	Ser	Leu	Lys
						245			250			255			
Thr	His	Pro	Leu	Trp	Arg	Leu	Trp	Lys	Lys	Ile	Trp	Ala	Val	Pro	Ser
						260		265			270				
Pro	Glu	Arg	Phe	Phe	Met	Pro	Leu	Tyr	Lys	Gly	Cys	Ser	Gly	Asp	Phe
						275		280			285				
Lys	Lys	Trp	Val	Gly	Ala	Pro	Phe	Thr	Gly	Ser	Ser	Leu	Glu	Leu	Gly
						290		295			300				
Pro	Trp	Ser	Pro	Glu	Val	Pro	Ser	Thr	Leu	Glu	Val	Tyr	Ser	Cys	His
						305		310			315			320	
Pro	Pro	Arg	Ser	Pro	Ala	Lys	Arg	Leu	Gln	Leu	Thr	Glu	Leu	Gln	Glu
						325			330			335			
Pro	Ala	Glu	Leu	Val	Glu	Ser	Asp	Gly	Val	Pro	Lys	Pro	Ser	Phe	Trp

YQ9263 CDS

	340	345	350
Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp			
355	360	365	
Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala			
370	375	380	
Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro			
385	390	395	400
Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp			
405	410	415	
Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser			
420	425	430	
Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg			
435	440	445	
Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro			
450	455	460	
Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser			
465	470	475	480
Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly			
485	490	495	
Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp			
500	505	510	
Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro			
515	520	525	
Pro Leu Ser Ser Pro Gly Pro Gln Ala Ser			
530	535		

<210> 3
<211> 2456
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (391)...(1977)

<400> 3

cagctgtctg cccacttctc ctgtggtgtg cctcacggtc acttgcttgt ctgaccgcaa	60
gtctgccat ccctggggca gccaactggc ctcagccgt gccccaggcg tgccctgtct	120
ctgtctggct gccccagccc tactgtcttc ctctgtgtag gctctgccc gatgccccgc	180
tggtcctcag cctcaggact atctcagcag tgactccctt gattctggac ttgcacctga	240
ctgaacctct gcccaccta aaccttcaacc tcccaccacc accactccga gtcccgctgt	300
gactcccacg cccaggagac cacccaagtg ccccaagcta aagaatggct ttctgaggaa	360
gatcctgaag gagtaggtct gggacacagc atg ccc cgg ggc cca gtg gct gcc	414
Met Pro Arg Gly Pro Val Ala Ala	
1	5

tta ctc ctg ctg att ctc cat gga gct tgg agc tgc ctg gac ctc act	462	
Leu Leu Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr		
10	15	20

tgc tac act gac tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg	510		
Cys Tyr Thr Asp Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg			
25	30	35	40

agc ccc aac ccc agc ata ctc agt ctc acc tgg caa gat gaa tat gag	558	
Ser Pro Asn Pro Ser Ile Leu Ser Leu Thr Trp Gln Asp Glu Tyr Glu		
45	50	55

DNA sequence

gaa ctt cag gac caa gag acc ttc tgc agc cta cac aag tct ggc cac Glu Leu Gln Asp Gln Glu Thr Phe Cys Ser Leu His Lys Ser Gly His 60 65 70	606
aac acc aca cat ata tgg tac acg tgc cat atg cgc ttg tct caa ttc Asn Thr Thr His Ile Trp Tyr Thr Cys His Met Arg Leu Ser Gln Phe 75 80 85	654
ctg tcc gat gaa gtt ttc att gtc aac gtg acg gac cag tct ggc aac Leu Ser Asp Glu Val Phe Ile Val Asn Val Thr Asp Gln Ser Gly Asn 90 95 100	702
aac tcc caa gag tgt ggc agc ttt gtc ctg gct gag agc atc aag cca Asn Ser Gln Glu Cys Gly Ser Phe Val Leu Ala Glu Ser Ile Lys Pro 105 110 115 120	750
gct ccc ccc ttg aac gtg act gtg gcc ttc tca gga cgc tat gat atc Ala Pro Pro Leu Asn Val Thr Val Ala Phe Ser Gly Arg Tyr Asp Ile 125 130 135	798
tcc tgg gac tca gct tat gac gaa ccc tcc aac tac gtg ctg aga ggc Ser Trp Asp Ser Ala Tyr Asp Glu Pro Ser Asn Tyr Val Leu Arg Gly 140 145 150	846
aag cta caa tat gag ctg cag tat cgg aac ctc aga gac ccc tat gct Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Leu Arg Asp Pro Tyr Ala 155 160 165	894
gtg agg ccg gtg acc aag ctg atc tca gtg gac tca aga aac gtc tct Val Arg Pro Val Thr Lys Leu Ile Ser Val Asp Ser Arg Asn Val Ser 170 175 180	942
ctt ctc cct gaa gag ttc cac aaa gat tct agc tac cag ctg cag atg Leu Leu Pro Glu Glu Phe His Lys Asp Ser Ser Tyr Gln Leu Gln Met 185 190 195 200	990
cgg gca gcg cct cag cca ggc act tca ttc agg ggg acc tgg agt gag Arg Ala Ala Pro Gln Pro Gly Thr Ser Phe Arg Gly Thr Trp Ser Glu 205 210 215	1038
tgg agt gac ccc gtc atc ttt cag acc cag gct ggg gag ccc gag gca Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ala Gly Glu Pro Glu Ala 220 225 230	1086
ggc tgg gac cct cac atg ctg ctg ctc ctg gct gtc ttg atc att gtc Gly Trp Asp Pro His Met Leu Leu Leu Ala Val Leu Ile Ile Val 235 240 245	1134
ctg gtt ttc atg ggt ctg aag atc cac ctg cct tgg agg cta tgg aaa Leu Val Phe Met Gly Leu Lys Ile His Leu Pro Trp Arg Leu Trp Lys 250 255 260	1182
aag ata tgg gca cca gtg ccc acc cct gag agt ttc ttc cag ccc ctg Lys Ile Trp Ala Pro Val Pro Thr Pro Glu Ser Phe Phe Gln Pro Leu 265 270 275 280	1230

tac agg gag cac agc ggg aac ttc aag aaa tgg gtt aat acc cct ttc Tyr Arg Glu His Ser Gly Asn Phe Lys Lys Trp Val Asn Thr Pro Phe 285 290 295	1278
acg gcc tcc agc ata gag ttg gtg cca cag agt tcc aca aca aca tca Thr Ala Ser Ser Ile Glu Leu Val Pro Gln Ser Ser Thr Thr Thr Ser 300 305 310	1326
gcc tta cat ctg tca ttg tat cca gcc aag gag aag aag ttc ccg ggg Ala Leu His Leu Ser Leu Tyr Pro Ala Lys Glu Lys Lys Phe Pro Gly 315 320 325	1374
ctg ccg ggt ctg gaa gag caa ctg gag tgt gat gga atg tct gag cct Leu Pro Gly Leu Glu Glu Gln Leu Glu Cys Asp Gly Met Ser Glu Pro 330 335 340	1422
ggc cac tgg tgc ata atc ccc ttg gca gct ggc caa gcg gtc tca gcc Gly His Trp Cys Ile Ile Pro Leu Ala Ala Gly Gln Ala Val Ser Ala 345 350 355 360	1470
tac agt gag gag aga gac cgg cca tat ggt ctg gtg tcc att gac aca Tyr Ser Glu Glu Arg Asp Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr 365 370 375	1518
gtg act gtg gga gat gca gag ggc ctg tgt gtc tgg ccc tgt agc tgt Val Thr Val Gly Asp Ala Glu Gly Leu Cys Val Trp Pro Cys Ser Cys 380 385 390	1566
gag gat gat ggc tat cca gcc atg aac ctg gat gct ggc cga gag tct Glu Asp Asp Gly Tyr Pro Ala Met Asn Leu Asp Ala Gly Arg Glu Ser 395 400 405	1614
ggc cct aat tca gag gat ctg ctc ttg gtc aca gac cct gct ttt ctg Gly Pro Asn Ser Glu Asp Leu Leu Leu Val Thr Asp Pro Ala Phe Leu 410 415 420	1662
tct tgc ggc tgt gtc tca ggt agt ggt ctc agg ctt gga ggc tcc cca Ser Cys Gly Cys Val Ser Gly Ser Gly Leu Arg Leu Gly Gly Ser Pro 425 430 435 440	1710
ggc agc cta ctg gac agg ttg agg ctg tca ttt gca aag gaa ggg gac Gly Ser Leu Leu Asp Arg Leu Arg Leu Ser Phe Ala Lys Glu Gly Asp 445 450 455	1758
tgg aca gca gac cca acc tgg aga act ggg tcc cca gga ggg ggc tct Trp Thr Ala Asp Pro Thr Trp Arg Thr Gly Ser Pro Gly Gly Ser 460 465 470	1806
gag agt gaa gca ggt tcc ccc cct ggt ctg gac atg gac aca ttt gac Glu Ser Glu Ala Gly Ser Pro Pro Gly Leu Asp Met Asp Thr Phe Asp 475 480 485	1854
agt ggc ttt gca ggt tca gac tgt ggc agc ccc gtg gag act gat gaa Ser Gly Phe Ala Gly Ser Asp Cys Gly Ser Pro Val Glu Thr Asp Glu 490 495 500	1902
gga ccc cct cga agc tat ctc cgc cag tgg gtg gtc agg acc cct cca	1950

卷之三

Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Arg Thr Pro Pro
 505 510 515 520
 cct gtg gac agt gga gcc cag agc agc tagcatataa taaccagcta 1997
 Pro Val Asp Ser Gly Ala Gln Ser Ser
 525
 tagtgagaag aggccctctga gcctggcatt tacagtgtga acatgttaggg gtgtgtgtgt
 gtgtgtgtgt ctgggttgtgt gtgttagcac atccatgttg ggatttggtc tggctatgt
 tatttggaaatgt ctaaattctc tacccaaagt tctaggccta cgagtgaatt ctatgttta
 caaacttgct gtgtaaacct tggcccttaa ttatatacca ttggttaaat aaaattggct
 gcaaccaatt actggagagg agaggagagg agaggagagg agaggagagg agaggctgcc
 gtgaggggag agggaccatg agcctgtggc caggagaaac agcaagtatc tgggttacac
 tggtagggag gtggccaggc cagcagttag aagagtagat taggggtgac ctccagtatt
 tgtcaaagcc aattaaaata aaaaaaaaaa aaaaaaagg 2057
 2117
 2177
 2237
 2297
 2357
 2417
 2456
 <210> 4
 <211> 529
 <212> PRT
 <213> Mus musculus
 <400> 4
 Met Pro Arg Gly Pro Val Ala Ala Leu Leu Leu Ile Leu His Gly
 1 5 10 15
 Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr
 20 25 30
 Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser
 35 40 45
 Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe
 50 55 60
 Cys Ser Leu His Lys Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr
 65 70 75 80
 Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val
 85 90 95
 Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe
 100 105 110
 Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val
 115 120 125
 Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu
 130 135 140
 Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu Gln Tyr Glu Leu Gln Tyr
 145 150 155 160
 Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile
 165 170 175
 Ser Val Asp Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys
 180 185 190
 Asp Ser Ser Tyr Gln Leu Gln Met Arg Ala Ala Pro Gln Pro Gly Thr
 195 200 205
 Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln
 210 215 220
 Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp Asp Pro His Met Leu Leu
 225 230 235 240
 Leu Leu Ala Val Leu Ile Ile Val Leu Val Phe Met Gly Leu Lys Ile
 245 250 255
 His Leu Pro Trp Arg Leu Trp Lys Lys Ile Trp Ala Pro Val Pro Thr
 260 265 270
 Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg Glu His Ser Gly Asn Phe

70 92 20 6 2 2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

	275	280	285
Lys Lys Trp Val Asn Thr Pro Phe Thr Ala Ser Ser Ile Glu Leu Val			
290	295	300	
Pro Gln Ser Ser Thr Thr Ser Ala Leu His Leu Ser Leu Tyr Pro			
305	310	315	320
Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro Gly Leu Glu Glu Gln Leu			
325	330	335	
Glu Cys Asp Gly Met Ser Glu Pro Gly His Trp Cys Ile Ile Pro Leu			
340	345	350	
Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser Glu Glu Arg Asp Arg Pro			
355	360	365	
Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Gly Asp Ala Glu Gly			
370	375	380	
Leu Cys Val Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro Ala Met			
385	390	395	400
Asn Leu Asp Ala Gly Arg Glu Ser Gly Pro Asn Ser Glu Asp Leu Leu			
405	410	415	
Leu Val Thr Asp Pro Ala Phe Leu Ser Cys Gly Cys Val Ser Gly Ser			
420	425	430	
Gly Leu Arg Leu Gly Gly Ser Pro Gly Ser Leu Leu Asp Arg Leu Arg			
435	440	445	
Leu Ser Phe Ala Lys Glu Gly Asp Trp Thr Ala Asp Pro Thr Trp Arg			
450	455	460	
Thr Gly Ser Pro Gly Gly Ser Glu Ser Ala Gly Ser Pro Pro			
465	470	475	480
Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Ala Gly Ser Asp Cys			
485	490	495	
Gly Ser Pro Val Glu Thr Asp Glu Gly Pro Pro Arg Ser Tyr Leu Arg			
500	505	510	
Gln Trp Val Val Arg Thr Pro Pro Pro Val Asp Ser Gly Ala Gln Ser			
515	520	525	
Ser			

<210> 5
<211> 551
<212> PRT
<213> Homo sapiens

	<400> 5		
Met Ala Ala Pro Ala Leu Ser Trp Arg Leu Pro Leu Leu Ile Leu Leu			
1	5	10	15
Leu Pro Leu Ala Thr Ser Trp Ala Ser Ala Ala Val Asn Gly Thr Ser			
20	25	30	
Gln Phe Thr Cys Phe Tyr Asn Ser Arg Ala Asn Ile Ser Cys Val Trp			
35	40	45	
Ser Gln Asp Gly Ala Leu Gln Asp Thr Ser Cys Gln Val His Ala Trp			
50	55	60	
Pro Asp Arg Arg Arg Trp Asn Gln Thr Cys Glu Leu Leu Pro Val Ser			
65	70	75	80
Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ala Pro Asp Ser Gln			
85	90	95	
Lys Leu Thr Thr Val Asp Ile Val Thr Leu Arg Val Leu Cys Arg Glu			
100	105	110	
Gly Val Arg Trp Arg Val Met Ala Ile Gln Asp Phe Lys Pro Phe Glu			
115	120	125	
Asn Leu Arg Leu Met Ala Pro Ile Ser Leu Gln Val Val His Val Glu			

5
4
3
2
1
0

130	135	140
Thr His Arg Cys Asn Ile Ser Trp Glu Ile Ser Gln Ala Ser His Tyr		
145	150	155
Phe Glu Arg His Leu Glu Phe Glu Ala Arg Thr Leu Ser Pro Gly His		160
165	170	175
Thr Trp Glu Ala Pro Leu Leu Thr Leu Lys Gln Lys Gln Glu Trp		
180	185	190
Ile Cys Leu Glu Thr Leu Thr Pro Asp Thr Gln Tyr Glu Phe Gln Val		
195	200	205
Arg Val Lys Pro Leu Gln Gly Glu Phe Thr Thr Trp Ser Pro Trp Ser		
210	215	220
Gln Pro Leu Ala Phe Arg Thr Lys Pro Ala Ala Leu Gly Lys Asp Thr		
225	230	235
Ile Pro Trp Leu Gly His Leu Leu Val Gly Leu Ser Gly Ala Phe Gly		
245	250	255
Phe Ile Ile Leu Val Tyr Leu Leu Ile Asn Cys Arg Asn Thr Gly Pro		
260	265	270
Trp Leu Lys Lys Val Leu Lys Cys Asn Thr Pro Asp Pro Ser Lys Phe		
275	280	285
Phe Ser Gln Leu Ser Ser Glu His Gly Gly Asp Val Gln Lys Trp Leu		
290	295	300
Ser Ser Pro Phe Pro Ser Ser Phe Ser Pro Gly Gly Leu Ala Pro		
305	310	315
Glu Ile Ser Pro Leu Glu Val Leu Glu Arg Asp Lys Val Thr Gln Leu		
325	330	335
Leu Leu Gln Gln Asp Lys Val Pro Glu Pro Ala Ser Leu Ser Ser Asn		
340	345	350
His Ser Leu Thr Ser Cys Phe Thr Asn Gln Gly Tyr Phe Phe His		
355	360	365
Leu Pro Asp Ala Leu Glu Ile Glu Ala Cys Gln Val Tyr Phe Thr Tyr		
370	375	380
Asp Pro Tyr Ser Glu Glu Asp Pro Asp Glu Gly Val Ala Gly Ala Pro		
385	390	395
Thr Gly Ser Ser Pro Gln Pro Leu Gln Pro Leu Ser Gly Glu Asp Asp		
405	410	415
Ala Tyr Cys Thr Phe Pro Ser Arg Asp Asp Leu Leu Leu Phe Ser Pro		
420	425	430
Ser Leu Leu Gly Gly Pro Ser Pro Pro Ser Thr Ala Pro Gly Gly Ser		
435	440	445
Gly Ala Gly Glu Glu Arg Met Pro Pro Ser Leu Gln Glu Arg Val Pro		
450	455	460
Arg Asp Trp Asp Pro Gln Pro Leu Gly Pro Pro Thr Pro Gly Val Pro		
465	470	475
Asp Leu Val Asp Phe Gln Pro Pro Pro Glu Leu Val Leu Arg Glu Ala		
485	490	495
Gly Glu Glu Val Pro Asp Ala Gly Pro Arg Glu Gly Val Ser Phe Pro		
500	505	510
Trp Ser Arg Pro Pro Gly Gln Gly Glu Phe Arg Ala Leu Asn Ala Arg		
515	520	525
Leu Pro Leu Asn Thr Asp Ala Tyr Leu Ser Leu Gln Glu Leu Gln Gly		
530	535	540
Gln Asp Pro Thr His Leu Val		
545	550	

<210> 6
<211> 539
<212> PRT

<213> Mus musculus

<400> 6
Met Ala Thr Ile Ala Leu Pro Trp Ser Leu Ser Leu Tyr Val Phe Leu
1 5 10 15
Leu Leu Leu Ala Thr Pro Trp Ala Ser Ala Ala Val Lys Asn Cys Ser
20 25 30
His Leu Glu Cys Phe Tyr Asn Ser Arg Ala Asn Val Ser Cys Met Trp
35 40 45
Ser His Glu Glu Ala Leu Asn Val Thr Thr Cys His Val His Ala Lys
50 55 60
Ser Asn Leu Arg His Trp Asn Lys Thr Cys Glu Leu Thr Leu Val Arg
65 70 75 80
Gln Ala Ser Trp Ala Cys Asn Leu Ile Leu Gly Ser Phe Pro Glu Ser
85 90 95
Gln Ser Leu Thr Ser Val Asp Leu Leu Asp Ile Asn Val Val Cys Trp
100 105 110
Glu Glu Lys Gly Trp Arg Arg Val Lys Thr Cys Asp Phe His Pro Phe
115 120 125
Asp Asn Leu Arg Leu Val Ala Pro His Ser Leu Gln Val Leu His Ile
130 135 140
Asp Thr Gln Arg Cys Asn Ile Ser Trp Lys Val Ser Gln Val Ser His
145 150 155 160
Tyr Ile Glu Pro Tyr Leu Glu Phe Glu Ala Arg Arg Arg Leu Leu Gly
165 170 175
His Ser Trp Glu Asp Ala Ser Val Leu Ser Leu Lys Gln Arg Gln Gln
180 185 190
Trp Leu Phe Leu Glu Met Leu Ile Pro Ser Thr Ser Tyr Glu Val Gln
195 200 205
Val Arg Val Lys Ala Gln Arg Asn Asn Thr Gly Thr Trp Ser Pro Trp
210 215 220
Ser Gln Pro Leu Thr Phe Arg Thr Arg Pro Ala Asp Pro Met Lys Glu
225 230 235 240
Ile Leu Pro Met Ser Trp Leu Arg Tyr Leu Leu Leu Val Leu Gly Cys
245 250 255
Phe Ser Gly Phe Ser Cys Val Tyr Ile Leu Val Lys Cys Arg Tyr
260 265 270
Leu Gly Pro Trp Leu Lys Thr Val Leu Lys Cys His Ile Pro Asp Pro
275 280 285
Ser Glu Phe Phe Ser Gln Leu Ser Ser Gln His Gly Asp Leu Gln
290 295 300
Lys Trp Leu Ser Ser Pro Val Pro Leu Ser Phe Phe Ser Pro Ser Gly
305 310 315 320
Pro Ala Pro Glu Ile Ser Pro Leu Glu Val Leu Asp Gly Asp Ser Lys
325 330 335
Ala Val Gln Leu Leu Leu Gln Lys Asp Ser Ala Pro Leu Pro Ser
340 345 350
Pro Ser Gly His Ser Gln Ala Ser Cys Phe Thr Asn Gln Gly Tyr Phe
355 360 365
Phe Phe His Leu Pro Asn Ala Leu Glu Ile Glu Ser Cys Gln Val Tyr
370 375 380
Phe Thr Tyr Asp Pro Cys Val Glu Glu Glu Val Glu Glu Asp Gly Ser
385 390 395 400
Arg Leu Pro Glu Gly Ser Pro His Pro Pro Leu Leu Pro Leu Ala Gly
405 410 415
Glu Gln Asp Asp Tyr Cys Ala Phe Pro Pro Arg Asp Asp Leu Leu Leu
420 425 430

Phe Ser Pro Ser Leu Ser Thr Pro Asn Thr Ala Tyr Gly Gly Ser Arg
 435 440 445
 Ala Pro Glu Glu Arg Ser Pro Leu Ser Leu His Glu Gly Leu Pro Ser
 450 455 460
 Leu Ala Ser Arg Asp Leu Met Gly Leu Gln Arg Pro Leu Glu Arg Met
 465 470 475 480
 Pro Glu Gly Asp Gly Glu Gly Leu Ser Ala Asn Ser Ser Gly Glu Gln
 485 490 495
 Ala Ser Val Pro Glu Gly Asn Leu His Gly Gln Asp Gln Asp Arg Gly
 500 505 510
 Gln Gly Pro Ile Leu Thr Leu Asn Thr Asp Ala Tyr Leu Ser Leu Gln
 515 520 525
 Glu Leu Gln Ala Gln Asp Ser Val His Leu Ile
 530 535

<210> 7
 <211> 522
 <212> PRT
 <213> Homo sapiens

<400> 7

Met Gly Leu Gly Arg Cys Ile Trp Glu Gly Trp Thr Leu Glu Ser Glu
 1 5 10 15
 Ala Leu Arg Arg Asp Met Gly Thr Trp Leu Leu Ala Cys Ile Cys Ile
 20 25 30
 Cys Thr Cys Val Cys Leu Gly Val Ser Val Thr Gly Glu Gly Gln Gly
 35 40 45
 Pro Arg Ser Arg Thr Phe Thr Cys Leu Thr Asn Asn Ile Leu Arg Ile
 50 55 60
 Asp Cys His Trp Ser Ala Pro Glu Leu Gly Gln Gly Ser Ser Pro Trp
 65 70 75 80
 Leu Leu Phe Thr Ser Asn Gln Ala Pro Gly Gly Thr His Lys Cys Ile
 85 90 95
 Leu Arg Gly Ser Glu Cys Thr Val Val Leu Pro Pro Glu Ala Val Leu
 100 105 110
 Val Pro Ser Asp Asn Phe Thr Ile Thr Phe His His Cys Met Ser Gly
 115 120 125
 Arg Glu Gln Val Ser Leu Val Asp Pro Glu Tyr Leu Pro Arg Arg His
 130 135 140
 Val Lys Leu Asp Pro Pro Ser Asp Leu Gln Ser Asn Ile Ser Ser Gly
 145 150 155 160
 His Cys Ile Leu Thr Trp Ser Ile Ser Pro Ala Leu Glu Pro Met Thr
 165 170 175
 Thr Leu Leu Ser Tyr Glu Leu Ala Phe Lys Lys Gln Glu Ala Trp
 180 185 190
 Glu Gln Ala Gln His Arg Asp His Ile Val Gly Val Thr Trp Leu Ile
 195 200 205
 Leu Glu Ala Phe Glu Leu Asp Pro Gly Phe Ile His Glu Ala Arg Leu
 210 215 220
 Arg Val Gln Met Ala Thr Leu Glu Asp Asp Val Val Glu Glu Glu Arg
 225 230 235 240
 Tyr Thr Gly Gln Trp Ser Glu Trp Ser Gln Pro Val Cys Phe Gln Ala
 245 250 255
 Pro Gln Arg Gln Gly Pro Leu Ile Pro Pro Trp Gly Trp Pro Gly Asn
 260 265 270
 Thr Leu Val Ala Val Ser Ile Phe Leu Leu Leu Thr Gly Pro Thr Tyr
 275 280 285

DRAFT

Leu Leu Phe Lys Leu Ser Pro Arg Val Lys Arg Ile Phe Tyr Gln Asn
290 295 300
Val Pro Ser Pro Ala Met Phe Phe Gln Pro Leu Tyr Ser Val His Asn
305 310 315 320
Gly Asn Phe Gln Thr Trp Met Gly Ala His Arg Ala Gly Val Leu Leu
325 330 335
Ser Gln Asp Cys Ala Gly Thr Pro Gln Gly Ala Leu Glu Pro Cys Val
340 345 350
Gln Glu Ala Thr Ala Leu Leu Thr Cys Gly Pro Ala Arg Pro Trp Lys
355 360 365
Ser Val Ala Leu Glu Glu Gln Glu Gly Pro Gly Thr Arg Leu Pro
370 375 380
Gly Asn Leu Ser Ser Glu Asp Val Leu Pro Ala Gly Cys Thr Glu Trp
385 390 395 400
Arg Val Gln Thr Leu Ala Tyr Leu Pro Gln Glu Asp Trp Ala Pro Thr
405 410 415
Ser Leu Thr Arg Pro Ala Pro Pro Asp Ser Glu Gly Ser Arg Ser Ser
420 425 430
Ser Ser Ser Ser Ser Asn Asn Asn Asn Tyr Cys Ala Leu Gly
435 440 445
Cys Tyr Gly Gly Trp His Leu Ser Ala Leu Pro Gly Asn Thr Gln Ser
450 455 460
Ser Gly Pro Ile Pro Ala Leu Ala Cys Gly Leu Ser Cys Asp His Gln
465 470 475 480
Gly Leu Glu Thr Gln Gln Gly Val Ala Trp Val Leu Ala Gly His Cys
485 490 495
Gln Arg Pro Gly Leu His Glu Asp Leu Gln Gly Met Leu Leu Pro Ser
500 505 510
Val Leu Ser Lys Ala Arg Ser Trp Thr Phe
515 520

<210> 8
<211> 468
<212> PRT
<213> Mus musculus

<400> 8
Met Ala Leu Gly Arg Cys Ile Ala Glu Gly Trp Thr Leu Glu Arg Val
1 5 10 15
Ala Val Lys Gln Val Ser Trp Phe Leu Ile Tyr Ser Trp Val Cys Ser
20 25 30
Gly Val Cys Arg Gly Val Ser Val Pro Glu Gln Gly Gly Gly Gln
35 40 45
Lys Ala Gly Ala Phe Thr Cys Leu Ser Asn Ser Ile Tyr Arg Ile Asp
50 55 60
Cys His Trp Ser Ala Pro Glu Leu Gly Gln Glu Ser Arg Ala Trp Leu
65 70 75 80
Leu Phe Thr Ser Asn Gln Val Thr Glu Ile Lys His Lys Cys Thr Phe
85 90 95
Trp Asp Ser Met Cys Thr Leu Val Leu Pro Lys Glu Glu Val Phe Leu
100 105 110
Pro Phe Asp Asn Phe Thr Ile Thr Leu His Arg Cys Ile Met Gly Gln
115 120 125
Glu Gln Val Ser Leu Val Asp Ser Gln Tyr Leu Pro Arg Arg His Ile
130 135 140
Lys Leu Asp Pro Pro Ser Asp Leu Gln Ser Asn Val Ser Ser Gly Arg
145 150 155 160

PROTEIN SEQUENCES

Cys Val Leu Thr Trp Gly Ile Asn Leu Ala Leu Glu Pro Leu Ile Thr
165 170 175
Ser Leu Ser Tyr Glu Leu Ala Phe Lys Arg Gln Glu Glu Ala Trp Glu
180 185 190
Ala Arg His Lys Asp Arg Ile Val Gly Val Thr Trp Leu Ile Leu Glu
195 200 205
Ala Val Glu Leu Asn Pro Gly Ser Ile Tyr Glu Ala Arg Leu Arg Val
210 215 220
Gln Met Thr Leu Glu Ser Tyr Glu Asp Lys Thr Glu Gly Glu Tyr Tyr
225 230 235 240
Lys Ser His Trp Ser Glu Trp Ser Gln Pro Val Ser Phe Pro Ser Pro
245 250 255
Gln Arg Arg Gln Gly Leu Leu Val Pro Arg Trp Gln Trp Ser Ala Ser
260 265 270
Ile Leu Val Val Val Pro Ile Phe Leu Leu Leu Thr Gly Phe Val His
275 280 285
Leu Leu Phe Lys Leu Ser Pro Arg Leu Lys Arg Ile Phe Tyr Gln Asn
290 295 300
Ile Pro Ser Pro Glu Ala Phe Phe His Pro Leu Tyr Ser Val Tyr His
305 310 315 320
Gly Asp Phe Gln Ser Trp Thr Gly Ala Arg Arg Ala Gly Pro Gln Ala
325 330 335
Arg Gln Asn Gly Val Ser Thr Ser Ala Gly Ser Glu Ser Ser Ile
340 345 350
Trp Glu Ala Val Ala Thr Leu Thr Tyr Ser Pro Ala Cys Pro Val Gln
355 360 365
Phe Ala Cys Leu Lys Trp Glu Ala Thr Ala Pro Gly Phe Pro Gly Leu
370 375 380
Pro Gly Ser Glu His Val Leu Pro Ala Gly Cys Leu Glu Leu Glu Gly
385 390 395 400
Gln Pro Ser Ala Tyr Leu Pro Gln Glu Asp Trp Ala Pro Leu Gly Ser
405 410 415
Ala Arg Pro Pro Pro Asp Ser Asp Ser Gly Ser Ser Asp Tyr Cys
420 425 430
Met Leu Asp Cys Cys Glu Glu Cys His Leu Ser Ala Phe Pro Gly His
435 440 445
Thr Glu Ser Pro Glu Leu Thr Leu Ala Gln Pro Val Ala Leu Pro Val
450 455 460
Ser Ser Arg Ala
465